# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/796,892

Source: IFWO

Date Processed by STIC: 3/22/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
*Effective 12/13/03*: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS.

http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

# Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 10 796,892 |
|---|---|---|

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

1_____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.

4_____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length

Sequence(s)_____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7_____Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)          SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11_____Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____ Misuse of n/Xaa

"n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

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**IFWO**

```
        RAW SEQUENCE LISTING                    DATE: 03/22/2004
        PATENT APPLICATION:  US/10/796,892      TIME: 11:47:18

        Input Set : A:\PTO.KD.txt
        Output Set: N:\CRF4\03222004\J796892.raw

     3 <110> APPLICANT: Han-Chung Wu
     4         Chin-Tarng Lin
     5         Tong-Young Lee
W--> 6 <120> TITLE OF INVENTION: A Peptide Marker Targeting To Nasopharyngeal Carcinoma Cell
And
W--> 7         Application Thereof
C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/796,892
C--> 8 <141> CURRENT FILING DATE: 2004-03-09
W--> 0 <130> FILE REFERENCE:
W--> 8 <160> NUMBER OF SEQ ID: 2
```

*(handwritten: "← please insert")*

*(handwritten: "delete →")*

*(handwritten: "please do not insert alpha Numeric headings.")*

*(handwritten: "Does Not Comply ... (pg. 1, 3)")*

```
ERRORED SEQUENCES

E--> 10 <210> SEQ ID NO  SEQ ID NO: 1
     11 <211> LENGTH: 12
     12 <212> TYPE: PRT
     13 <213> ORGANISM: Artificial Sequence
     15 <220> FEATURE:
     16 <223> OTHER INFORMATION: The Peptide Maker Targeting To Nasopharyngeal Carcinoma Cell
E--> 18 <400> SEQUENCE: 1
     19 Arg Leu Leu Asp Thr Asn Arg Pro Leu Leu Pro Tyr
E--> 20 1       5       10
E--> 22 <210> SEQ ID NO:  SEQ ID NO: 2
     23 <211> LENGTH: 3
     24 <212> TYPE: PRT
     25 <213> ORGANISM: Artificial Sequence
     27 <220> FEATURE:
     28 <223> OTHER INFORMATION: The Peptide Maker Targeting To Nasopharyngeal Carcinoma Cell
E--> 30 <400> SEQUENCE: 2
     31 Leu Pro Tyr
     32 1
```

*(handwritten: "delete, same error")*

*(handwritten: "please see item #3 on error summary sheet.")*

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 03/22/2004
PATENT APPLICATION:  US/10/796,892      TIME: 11:47:19

Input Set  : A:\PTO.KD.txt
Output Set: N:\CRF4\03222004\J796892.raw

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:0; Line(s) 6

**VERIFICATION SUMMARY**
PATENT APPLICATION:  **US/10/796,892**

DATE: 03/22/2004
TIME: 11:47:19

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\03222004\J796892.raw**

L:6 M:283 W: Missing Blank Line separator, <120> field identifier
L:8 M:270 C: Current Application Number differs, Replaced Current Application No
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:8 M:283 W: Missing Blank Line separator, <160> field identifier
L:10 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:18 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:1
L:20 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:22 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:30 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:2